--39. An isolated polynucleotide comprising a sequence region that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2.

40. The isolated polynucleotide of claim 39, wherein said sequence region comprises at least 21 contiguous nucleotides from nucleotide 122 to nucleotide 970 of SEQ ID NO:1.

41. The isolated polynucleotide of claim 40, wherein said sequence region comprises at least 30 contiguous nucleotides from nucleotide 122 to nucleotide 970 of SEQ ID NO:1.

42. The isolated polynucleotide of claim 41, wherein said sequence region comprises at least 40 contiguous nucleotides from nucleotide 122 to nucleotide 970 of SEQ ID NO:1.

43. The isolated polynucleotide of claim 42, wherein said sequence region comprises the sequence from nucleotide 122 to nucleotide 970 of SEQ ID NO:1.

44. The isolated polynucleotide of claim 42, comprising the sequence of SEQ ID NO:1.

45. The isolated polynucleotide of claim 39, wherein said polypeptide promotes melanoma senescence.

46. The isolated polynucleotide of claim 39, wherein said polypeptide suppresses glioma cell tumor generation.

47. The isolated polynucleotide of claim 39, wherein said polynucleotide is from about 849 to about 5,000 basepairs in length.

48. The isolated polynucleotide of claim 47, wherein said polynucleotide is from about 849 to about 3,000 basepairs in length.

49. The isolated polynucleotide of claim 48, wherein said polynucleotide is from about 849 to about 1,000 basepairs in length.

50. The isolated polynucleotide of claim 39, wherein said coding region is operably positioned under the control of a promoter.

51. The isolated polynucleotide of claim 39, wherein said coding region is operatively linked to a second coding region that encodes a selected peptide or polypeptide, said polynucleotide encoding a methylthioadenosine phosphorylase fusion peptide or polypeptide.

52. The isolated polynucleotide of claim 39, comprised within a vector.

53. The isolated polynucleotide of claim 39, comprised within a host cell.

54. A nucleic acid of from about 850 to about 10,000 nucleotides in length comprising a gene encoding a methylthioadenosine phosphorylase polypeptide, said polypeptide comprising a sequence region of at least about 10 contiguous residues from SEQ ID NO:2.

55. The nucleic acid of claim 54, wherein said polypeptide comprises a sequence region of at least about 20 contiguous residues from SEQ ID NO:2.

56. The nucleic acid of claim 55, wherein said polypeptide comprises a sequence region of at least about 30 contiguous residues from SEQ ID NO:2.

57. The nucleic acid of claim 54, wherein said gene is operably linked to a heterologous promoter.

69. The vector of claim 67, comprised within a host cell.

70. A host cell comprising at least a first gene that encodes a mammalian methylthioadenosine phosphorylase polypeptide comprising the amino acid sequence of SEQ ID NO:2.

71. The host cell of claim 70, wherein said gene comprises the nucleic acid sequence of from about nucleotide 122 to nucleotide 970 of SEQ ID NO:1.

72. The host cell of claim 70, wherein said cell is a prokaryotic host cell.

73. The host cell of claim 70, wherein said cell is a eukaryotic host cell.

74. An isolated polynucleotide comprising a nucleic acid sequence that encodes a methylthioadenosine phosphorylase polypeptide, wherein said isolated polynucleotide hybridizes to an at least 21 nucleotide contiguous nucleic acid sequence from SEQ ID NO:1 under stringent hybridization conditions.

75. The isolated polynucleotide of claim 74, wherein said polypeptide comprises a contiguous amino acid sequence from SEQ ID NO:2.

76. The isolated polynucleotide of claim 74, wherein said isolated polynucleotide encodes a human methylthioadenosine phosphorylase polypeptide.

77. A method of making a methylthioadenosine phosphorylase polypeptide, comprising the steps of:

(a) obtaining a vector in which a gene encoding a polypeptide comprising a sequence region of at least about 10 contiguous amino acid residues from SEQ ID NO:2 is positioned under the control of a promoter;

58. The nucleic acid of claim 57, wherein said promoter is selected from the group consisting of a RSV, CMV, LTR, Sv40, *lac*, *trp*, *tac*, lacUV5, and a T7 promoter.

59. The nucleic acid of claim 57, comprised within a vector.

60. The nucleic acid of claim 57, comprised within a host cell.

61. An isolated nucleic acid segment of between about 21 and about 500 nucleotides in length that comprises a contiguous sequence from SEQ ID NO:1, or that specifically hybridizes to said contiguous sequence from SEQ ID NO:1 under stringent hybridization conditions.

62. The nucleic acid segment of claim 61, wherein said segment is between about 21 and about 300 nucleotides in length.

63. The nucleic acid segment of claim 62, wherein said segment is between about 21 and about 200 nucleotides in length.

64. The nucleic acid segment of claim 63, wherein said segment is between about 21 and about 100 nucleotides in length.

65. The nucleic acid segment of claim 61, comprised within a vector.

66. The nucleic acid segment of claim 61, comprised within a host cell.

67. A vector comprising at least a first gene that encodes a mammalian methylthioadenosine phosphorylase polypeptide comprising the amino acid sequence of SEQ ID NO:2.

68. The vector of claim 67, wherein said gene comprises the nucleic acid sequence of SEQ ID NO:1.

(b) introducing said vector into a host cell;

(c) culturing said host cell under conditions effective to express said polypeptide; and

(d) collecting said expressed polypeptide.

78. A method for detecting a nucleic acid segment comprising a sequence region encoding a methylthioadenosine phosphorylase polypeptide, comprising the steps of:

(a) obtaining sample nucleic acids suspected of containing a sequence region encoding a methylthioadenosine phosphorylase polypeptide;

(b) contacting said sample nucleic acids with a nucleic acid segment comprising at least 21 contiguous nucleotides of SEQ ID NO:1 under conditions effective to allow hybridization of substantially complementary nucleic acids; and

(c) detecting the hybridized complementary nucleic acids thus formed.

79. The method of claim 78, wherein the sample nucleic acids contacted are located within a cell.

80. The method of claim 78, wherein the sample nucleic acids are separated from a cell prior to contact.

81. The method of claim 78, wherein the sample nucleic acids are DNA.

82. The method of claim 78, wherein said isolated nucleic acid segment comprises a detectable label and the hybridized complementary nucleic acids are detected by detecting said label.

83. The method of claim 82, wherein the nucleic acid segment comprises a radio-, enzymatic or fluorescent label.

84. A detection kit comprising, in suitable container means, a first nucleic acid segment comprising at least 21 contiguous nucleotides of SEQ ID NO:1 and a detection reagent.

85. The detection kit of claim 84, further comprising at least a first restriction endonuclease.

86. The detection kit of claim 84, further comprising a second nucleic acid segment comprising at least 21 contiguous nucleotides of SEQ ID NO:1.

87. The detection kit of claim 84, wherein said detection reagent is a detectable label that is linked to said nucleic acid segment.

88. An isolated nucleic acid that:

(a) comprises a sequence region that consists of at least 21 contiguous nucleotides that have the same sequence as, or are complementary to, 21 contiguous nucleotides of SEQ ID NO:1; or

(b) is a nucleic acid of from 21 to 10,000 nucleotides in length that hybridizes to a contiguous nucleotide sequence from SEQ ID NO:1; or the complement thereof, under stringent hybridization conditions.

89. The isolated nucleic acid of claim 88, that comprises a sequence region that consists of at least 14 contiguous nucleotides that have the same sequence as, or are complementary to, 21 contiguous nucleotides of SEQ ID NO:1.

90. The isolated nucleic acid of claim 88, that is from 21 to 10,000 nucleotides in length that hybridizes to a contiguous nucleotide sequence from SEQ ID NO:1, or the complement thereof, under stringent hybridization conditions.

91. The isolated nucleic acid of claim 88, wherein said nucleic acid is up to 10,000 basepairs in length.

92. The isolated nucleic acid of claim 91, wherein said nucleic acid is up to 5,000 basepairs in length.

93. The isolated nucleic acid of claim 92, wherein said nucleic acid is up to 3,000 basepairs in length.

94. The isolated nucleic acid of claim 93, wherein said nucleic acid is up to 1,000 basepairs in length.

95. A method of identifying a cancer type, comprising determining a pattern of homozygous deletions in the methylthioadenosine phosphorylase gene on human chromosome 9p21, and associating said pattern with the pattern obtained from the particular cancer sought to be identified.

96. The method of claim 95, wherein said cancer is identified as a tumor cell, a leukemia, a glioma, a melanoma, bladder cancer, brain cancer, breast cancer, lung cancer, ovarian cancer, or pancreatic cancer.

## REMARKS

The active claims in this case are claims 39-96.

This application is being filed herewith as a continuation under 37 C.F.R. § 1.53(d) of application Serial No. 08/674,311, filed July 1, 1996. Application Serial No. 08/674,311 is a continuation-in-part of application Serial No. 60/000,831, filed July 2, 1995. The specification has been amended to recite the relationship with the parent case, Serial No. 60/000,831, filed July 2, 1995.